

Figure 2

M A V L G L L F C L V T F P S C
ATG GCT GTC TTG GGG CTG CTC TTC TGC CTG GTG ACA TTC CCA AGC TGT
V L S
GTC CTG TCC (-1 to -19, Leader)

Q V Q V K E S G P F L V P P S Q
CAG GTG CAG GTG AAG GAG TCA GGA CCT TTC CTG GTG CCC CCC TCA CAG
S L S I T C T V S G F S L T
AGC CTG TCC ATC ACA TGC ACT GTC TCA GGG TTC TCA TTA ACC
(1-30, Frame work 1)

T Y G V S
ACC TAT GGT GTA AGC (31-35, CDR 1)

W I R Q P P G K G L E W L G
TGG ATT CGC CAG CCT CCA GGA AAG GGT CTG GAG TGG CTG GGA
(36-49, Frame work 2)

A I W G D G T T N Y H S A L I S
GCA ATT TGG GGT GAC GGG ACC ACA AAT TAT CAT TCA GCT CTC ATA TCC
(50-65, CDR 2)

R L S I S K D N S K S Q V F L K
AGA CTG AGC ATC AGC AAG GAT AAC TCC AAG AGC CAA GTT TTC TTA AAA
L N S L Q T D D T A T Y Y C A K
CTG AAC AGT CTG CAA ACT GAT GAC ACG GCC ACG TAC TAC TGT GCC AAA
(66-97, Frame work 3)

L G N Y D A L D W Y
CTG GGT AAC TAC GAT GCT CTG GAC TAC
(98-106, CDR 3)

W G Q G T S V T V S S
TGG GGT CAA GGA ACC TCA GTC ACC GTC TCC TCA
(107-117, Frame work 4)

A K T T P P P V Y P L V P G S L
GCC AAA ACG ACA CCC CCA CCC GTC TAT CCA TTG GTC CCT GGA AGC TTG GG
(Constant region)

Figure 3(B)

1A7: 1 QVQVKESGPFLVPPSQSLITCTVSGFSLTTYGVSWIRQPPGKLEWLGAIWGDGTTNYH 60

| | | | |
|----|-----|--------------------------------------------|-----|
| 1 | 1 | .G.A.....S....V.....V....S.... | 52 |
| 2 | 1 | ...LQ...G.A.....S..IT.V.....V:....N.... | 60 |
| 3 | 20 | ...L....G.A.....G...N.V.....T...N.S.D.N | 79 |
| 4 | 1 | ...L.T.G.A.....S...H.V.....VV..S..S...N | 60 |
| 5 | 1 | ...L....G.A.....S...H.V.....V..AG.S...N | 60 |
| 6 | 1 | ...L....G.A.....S...H.V.....V..AG.S...N | 60 |
| 7 | 1 | ...L....G.A.....P..S...D.V.....V...G.S...N | 60 |
| 8 | 23 | ...LQ...G.A.....G...N.V.....M....N.D.N | 82 |
| 9 | 1 | ...L....G.A.....G...N.V.....M....N.D.N | 60 |
| 10 | 133 | ...LQ...G.A.....G...N.V.....M....N.D.N | 192 |
| 11 | 20 | ...L....G.A.....G...N.V.....M....N.D.N | 79 |
| 12 | 1 | ...L....G.A.....SR.S.H.V.....M...G.N.D.N | 60 |
| 13 | 21 | .HL....V.A.....N...H.V.....V..AG.N...N | 80 |
| 14 | 23 | ...LQ...G.A.....G...N.V.....M....N.D.N | 82 |
| 15 | 1 | ...LQ...G.A.....G...N.V.....M....N.D.N | 60 |

1A7: 61 SALISRLSISKDNSKSQVFLKLSLQTTDDTATYYCAKL-----GNYDALB^{DYWG}QGTSVTVSS 117

| | | | |
|----|-----|--------------------------------------------------------------|-----|
| 1 | 53 |P-----YDYExxxxx ^YTL.. | 109 |
| 2 | 61 |x-----xxxxxxx.K ^Y | 120 |
| 3 | 80 | .T.K...T.T.....M.....R...SVSIYYYGRSDK.FT. ^Y | 144 |
| 4 | 61 | ...K.....M.....M...Rx-----xx.D.Y.M ^Y | 119 |
| 5 | 61 | ...M.....M.....M...Rx-----xxxxxx.Y.M ^Y | 120 |
| 6 | 61 | ...M.....M.....M...Rx-----xxx.Y.M ^Y | 118 |
| 7 | 61 | ...M.....M..X...M...xx-----xxx.X.Y.M ^Y | 119 |
| 8 | 83 | ...K.....M..H...R...RE-----RDYR. ^YT.... | 138 |
| 9 | 61 | ...K.....M..H...R...RE-----RDYR. ^YTL.... | 116 |
| 10 | 193 | ...K.....M..H...R...RE-----RDYR. ^YT.... | 248 |
| 11 | 80 | ...K.....M..H...R...RE-----RDYR. ^YTL.... | 135 |
| 12 | 61 | ...K.....M.....M...RD-----GYDx.M ^Y | 117 |
| 13 | 81 | ...M.....M...I...I...x-----xxxxx.Y.M ^Y | 139 |
| 14 | 83 | ...K.....M..H...R...RE-----RDYR. ^YT.... | 138 |
| 15 | 61 | ...K.....M..H...R...RE-----RDYR. ^YT.... | 116 |

Figure 3(C)

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VL consensus: 1 DVLMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKKGQSPKLLIYFVSNRF 60
1A7:          1 .....P.....N..... 60

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VL consensus: 61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHPVTFGGGTKLEIK 112
1A7:          61 ..... 112

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VH consensus: 1 QVQLKESGPGLVAPSQLSITCTVSGFSLTSYGVHWVRQPPGKGLEWLGVIWGDGSTNYN 60
1A7:          1 ...V.....F..P.....T...S.I.....A.....T...H 60

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VH consensus: 61 SALKSRLSISKDNSKSQVFLKMNSLQTDATARYYCARExxxxYYAMDYWGQTSVTVSS 119
1A7:          61 ...I.....L.....T....KL--GN.D.LD..... 117

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